

A deep amplicon sequencing study of the algal communities in lacustrine and hydro-terrestrial environments of Antarctica

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Antarctica's organisms live primarily in the coastal, ice-free areas which cover approximately 0.18% of the continent's surface. Members of Cyanobacteria and eukaryotic algae are important primary producers in Antarctica since they can synthesize organic compounds from carbon dioxide and water using solar energy. However, community structures of photosynthetic algae in Antarctica have not yet been fully explored at molecular level. We collected diverse algal samples in lacustrine and hydro-terrestrial environments of Langhovde and Skarvsnes (Figure 1), which are two ice-free regions in East Antarctica. We performed deep amplicon sequencing of both 16S ribosomal ribonucleic acid (rRNA) and 18S rRNA genes, and we explored the distribution of sequence variants of these genes at single nucleotide difference resolution (Ref. 1). Based on the obtained data, we discuss the detailed structures of the algal communities in Langhovde and Skarvsnes regions. In addition, we observed a decrease of sequence quality in samples containing a specific combination of indexes, namely N704 and S507 in widely used Nextera dual index kits, in multiple runs on the Illumina MiSeq sequencer. We observed significant decreases in α -diversity caused by this specific index combination, resulting from loss of low-abundance sequence variants during denoising (Ref. 2). Therefore, we suggest cautious interpretation of “denoised” microbiome data containing low-quality sequence reads.

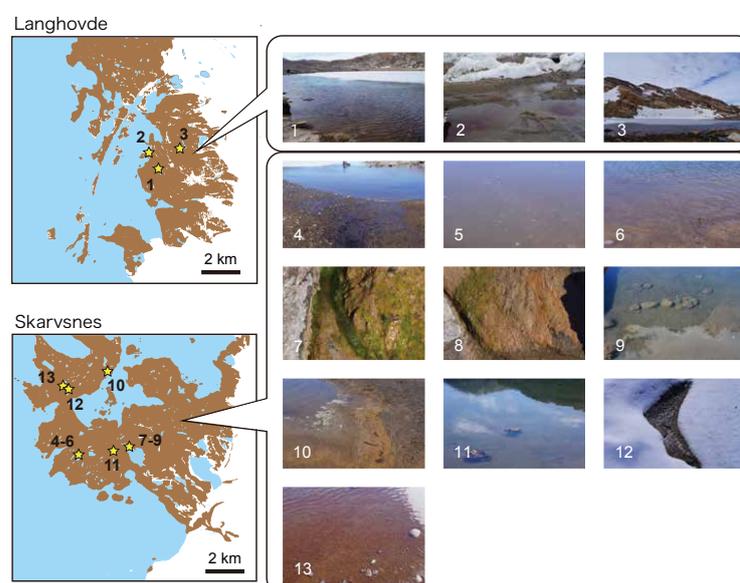


Figure 1. Sampling points in this study.

References

- 1, Hirose, Y., Shiozaki, T., Otani, M., Kudoh, S., Imura, S., Eki, T., Harada, N. Investigating algal communities in lacustrine and hydro-terrestrial environments of East Antarctica using deep amplicon sequencing. *Microorganisms*, 8(4), 497, 2020.
- 2, Hirose Y, Shiozaki T, Hamano I, Yoshihara S, Tokumoto H, Eki T, Harada N. A specific combination of dual index adaptors decreases the sensitivity of amplicon sequencing with the Illumina platform. *DNA Res.* in press. 2020.